

OM of: US-08-482-402A-3_COPY_1_848 to: Issued_Patents_NA: * out_format : pfs
 Date: Nov 26, 2001 11:25 AM
 About: Results were produced by the GenCore software, version 4.5.
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Command line parameters:

```
-MODEL=frame+pan.model -DEV=xlh
-DB_Issued_Patents_NA_QFNTI.fasta -PCTUSPOOL/USPTO_spool/runat_26112001_091652_29072/app_query.fasta_1.931
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPWT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXPT=7.000 -START=1 -MATRIX=diosum62
-TRANS=human40 cdi -LIST=45 -DOCAALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=100 -MINLEN=0 -MAXLEN=2000000000
-USER=US08A82402 @CGNL_1.82 -ICPU=6 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLDPXY -WAIT -THREADS=1
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Search information block:

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Query: US-08-482-402A-3_COPY_1_848
Query length: 848
Database: Issued_Patents_NA: *
Database sequences: 351203
Database length: 113238999
Search time (sec): 52.770000
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score_list:

Sequence	Strd	Orig	Zscore	Escore	Len	Documentation
/cgn2_6/podata/2/ina/5B_COMB.seq:US-08-313-200-2+	4528.00	759.20	0.0	3048		
/cgn2_6/podata/2/ina/PCTUS_COMB.seq:US-08-3837-2+	4528.00	759.20	0.0	3048		
/cgn2_6/podata/2/ina/backfiles1.seq:PCTUS_COMB.seq:US-08-313-200-2+	4528.00	759.20	0.0	3048		
/cgn2_6/podata/2/ina/backfiles1.seq:5460961-1-4+	1576.50	2617.93	3.6e-138	2261	Pate	
/cgn2_6/podata/2/ina/backfiles1.seq:5460961-5-4+	1509.50	2505.94	6.2e-132	2097	Pate	
/cgn2_6/podata/2/ina/6A_COMB.seq:US-08-840-551-6+	396.00	655.48	7.3e-29	262	g	
/cgn2_6/podata/2/ina/6A_COMB.seq:US-08-840-551-6+	396.00	430.17	2.6e-16	169	g	
/cgn2_6/podata/2/ina/6A_COMB.seq:US-08-911-853-29+	202.50	274.90	1.2e-07	17612		
/cgn2_6/podata/2/ina/6A_COMB.seq:US-08-911-853-29+	202.50	274.90	1.2e-07	17612		
/cgn2_6/podata/2/ina/6A_COMB.seq:US-08-911-853-16+	195.00	286.28	2.7e-08	2742		
/cgn2_6/podata/2/ina/6A_COMB.seq:US-09-479-409-16+	195.00	286.28	2.7e-08	2742		
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; VOLUME: 84
; PAGES: 5555-5559
; DATE: 1987
; RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 3048
US-08-313-200-2

alignment_scores:
Quality: 4528.00 Length: 848
Ratio: 5.365 Gaps: 0
Percent Similarity: 99.528 Percent Identity: 99.175

alignment_block:
US-08-482-402A-3_COPY_1_848 x US-08-313-200-2 ..

Align seg 1/1 to: US-08-313-200-2 from: 1 to: 3048

1 Met Arg Ala Leu Ala Val Leu Ser Val Thr Leu Val Met Ala Cys Thr Gln 17
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
73 ATGAGCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCAAGAA

17 ual aPhepheProPheleSerArg Gly Lys Glu Leu LeutrpGlyLysP 34
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
123 AGCTTCTTCCCTTCATCCTCGAGAGGAAAGAACCTCTTGGAAAGC 172

34 rogluGluSerArgValSerSerValLeuGluGluSerLysArgLeuVal 50
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
173 CTGGGGACTCTCGTGTCTCTAGGGCTTGAGGAAGGGCTGTGTG 222

51 Asp Thra Ala Met Trp Ala thr Met Glu Arg Asn Leu Lys Ly Arg Gly I I 67
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
223 GACACCGCCATGTA CGCCACAGTGCAGAGAAACCTCAAGAAAAGGAAAT 272

67 eue Ser Gly Ala Glu Leu Leu Ser Gly Ser ProGlu ProHrs 84
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
273 CCTTTCTCAGCTCAGCTCTGCTCTTCCAAACATTCCTGAGCACCAA 322

84 erglyValleAla Arg Ala Ala Glu Leu Met Glu thr SerIleGlnAla 100
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
323 GCGGAGTATGCCGAGCAGAGATAATCGAACATCAAGCG 372

101 Met Lys Arg Lys Val Asn Leu Lys Thr Glu Gln Ser Gln His Pro Thr As 117
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
373 ATGAAAAGAAAGTCAAACCTGAAACTCAACATCACAGCATCARRCGGA 422

117 Pal Leu Ser Glu Asp Ile Ala Arg Ser Leu Ala Asn Lys 150
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
473 TCCCTTACATGCTGCCCAAAATGCCAAACACTGCCGAAACAA 522

134 euProTyMetLeuProProLyScsProAsnThrCysLeuAlaAsnLys 150
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
423 TGTATTACAGAAGATCTGCTGACATCATGCAAACTGCAAGCTGATGTC 472

167 yala Ser Asn Thr Ala Leu Ala Arg TriPheLeu ProProVal Tyr Gln IysP 184
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573 CGCTCTAACACGGCCCTGGCACAGTCAGCTCCCTCAACTCTATGAGGAGC 622

184 IyPheSerGlnProArgGlyTriPheLeu ProGlyPheLeu Tyr Asn Gln IysPhe 200
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
623 GCCTCACTCAGGCCGAGGCTGGAAACCCGGCTTGACACGGTT 672

201 ProLeu ProProVal Arg Gly IysPheLeu Val Gln Val Ser As 217
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
673 CCAC TGCCCCGTCAGGAGTCAGACATGCTATCAAGTTCAA 722

217 nGlu Val Thr Asp SpasPaspArg Tyr Ser Asp Leu Met Ala Arg Trp G 234
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723 TGAGGTTGTCACAGATGATGACCGCTATTCTGACATCTCTGATGGCATGG 772

234 lyGln Tyr Ile Asp His Asp Ile Ala Phe Thr ProGln Ser Thr Ser Lys 250
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
773 GACAATACATCGACCACGAAATCGCTTCACCAAGACGACCAAA 822

251 Ala Ala Phe HeI Gly Lys Ser Asp Cys Glu Asp Gln Asn 267
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
823 GCTGCCTTCGGGGGGGGGGTGACTGCCCAGATGACTTGAGAACCAA 872

267 nProCysPheProIleGlnLeuProGlu Ile Ala Arg Pro Ala Ala Gln IysP 284
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
873 CCCATGTTTCCATACAACCTCCAGGAGGGCCGGCCGGCA 922

284 hrAlaCys Ile ProPhe Tyr Arg Ser Ser Ala Ala Cys Gln IysPhe Gln IysP 300
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
923 CCGCTGTGCGCCCTCTACCGCTTCGCGCTCGGCACCGGGAC 972

317 tasnGlyLeuThrSerPheLeuAspIleSerThrValtyrGlySerSerP 334
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1023 GAACGGGTGACCTCTGTTCTGGACCGTGTACCGTGTATGGACGCTCC 1072

334 roAlaLeuGluArgGlnIleArgAsnTrpIhrSerAlaGluGlyLeuLeu 350
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1073 CGGCCCTAGAGGGAGCTGGAACTGGACAGTCGAACTGGCCAGGCTGTC 1122

351 Arg Val His Gly Ile Arg Leu Arg Asn Trp IhrSerAlaGluGlyLeuLeu 367
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367 lProProArgAlaProAlaLacysAlaProGluProGlyAsnProGlyG 384
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417 uAlaAlaAlaLeuLysAlaLeuAsnAlaHisIleIlePheSerIaAspAlaIaL 434
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434 yrGlnGluAlaArgLysValValGlyAlaLysLeuHisGlnIleIleIleIle 450
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451 Arg Asp Tyr Ile ProArg Ile Leu Gly ProGlu Ala Phe Gln Gln Iuvalryva 467
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1423 AGGGATTACTCCCCAGGATCTGGGACGGCCAGGCTCTCAGGACTACGT 1472

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seq_documentation_block:
sequence 2, Application PC/TUS9303837
GENERAL INFORMATION:
APPLICANT: Baker, Jr., James R.
APPLICANT: Reniq, Ronald J.
TITLE OF INVENTION: Thyroid Peroxidase Epitopic Regions
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: USA
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03837
FILING DATE: 19930422
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lewak, Anna M.
REGISTRATION NUMBER: 33006
REFERENCE/DOCKET NUMBER: 2115-00658PFA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 641-1600
TELEFAX: (313) 641-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3008 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: Linear
MOLECULE TYPE: mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Mature
TISSUE TYPE: Thyroid gland (from patients with
Grave's disease)
IMMEDIATE SOURCE:
CLONE: Phto-2.8
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 2pter-q11
PUBLICATION INFORMATION:
AUTHORS: Kimura, S.
AUTHORS: Kotani, T.
AUTHORS: McBride, O. W.
AUTHORS: Umeki, K.
AUTHORS: Nakayana, T.
AUTHORS: Ohnaki, S.
AUTHORS: Hirai, K.
TITLE: Human thyroid peroxidase: Complete cDNA and
protein sequence, chromosome mapping, and
identification of two alternatively spliced mRNAs
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 84
PAGES: 5555-5559
DATE: 1987
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 3048
PCT-US93-03837-2
alignment_scores: Quality: 4528.00
Length: 848

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Percent Similarity:	99.528	Percent Identity:	99.175
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123 AGCCCTCTCCCTCATCTCGAGGGAAAGAACTCTTGGGAAA			
34 roGluGluSerArgValSerValLeuGluSerLysArgLeuV			
173 CTGAGAGTCCTGCTCTACGTCGTTGGAGAAAGCAAGGCCTGGGAA			
51 AspThrAlaMetTyrAlaThrMetGlnArgAsnLeuLysLysArgGly			
223 GACACGCCATTGACCCACAGTCAGTGACAGAAACCTCAACAAAAGAGGA			
67 eLeuSerGlyAlaGlnLeuLeuSerPheSerLysLeuProGluLeuProGluLeu			
273 CCTCTTCCAGCTCAGCTTCAGTCAGTCAGTCAGTCAGAAACTTCTGAGGCCAAC			
84 erglyvalineAlaArgAlaAlaGluIleMetGluThrSerIleGlnA			
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101 MetLysArgLysValAsnLeuLysThrGlnGlnSerGlnHisProThrHis			
373 ATGAAAAGAAAGTCAACCTGAAACTCAACATACTCACACCATCCAAACGG			
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 seq_documentation_block:
 ; Patent No. 5469961
 ; APPLICANT: DEBY, CAROL; PINCEMAIL, JOEL; BOLLEN, ALEX
 ; TITLE OF INVENTION: HUMAN MYELOPEROXIDASE AND ITS
 ; THERAPEUTIC APPLICATION

213 eGlnValSerAsnGluValValThrAspAspAspArgTyrSerAspLeu 230
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seq_documentation_block:

; Patent No. 5460961.

; APPLICANT: DEFY, CAROL; PINCEMAIL, JOEL; BOLLEN, ALEX

; TITLE OF INVENTION: HUMAN MYELOPEROXIDASE AND ITS

; THERAPEUTIC APPLICATION

; NUMBER OF SEQUENCES: 13

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/641,678

; FILING DATE: 16-JAN-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 460-931

; FILING DATE: 14-FEB-1990

; LENGTH: 2097

5460961-4

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109 hrGlnGlnSerGlnHisProThrAspAlaLeuSerGluAspIleLeu 125
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142 sProAsnThrCysLeuAlaAsnLysThrArgProIleGlyAlaCysA 159
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seq_documentation_block:

; Sequence 6, Application US/08840551B

; Patent No. 6066449

; GENERAL INFORMATION:

; APPLICANT: Ditzkoff, Beth A., et al.

; TITLE OF INVENTION: METHOD OF DETECTING METASTATIC THYROID CANCER

; FILE REFERENCE: 0575/51662/jpw/jkm

; CURRENT APPLICATION NUMBER: US/08/840,551B

; CURRENT FILING DATE: 1997-04-15

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 169

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: OTHER

; OTHER INFORMATION: ACID

US-08-840-551-6

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 1 GTCCTTGAGANAGANGCCCTGGCATGAGCTGCGATGCGATGAT 50

58 tGluArgAsnLeuLysArgGlyIleLeuSerGlyAlaGlnLeuLeus 75
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seq_documentation.block:

Sequence 29, Application US/08911853
 Patent No. 6048710
 GENERAL INFORMATION:
 APPLICANT: Gerritse, Gijsbert
 APPLICANT: Quax, Wilhelmus J.
 TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genencor International
 STREET: 925 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTY: USA
 ZIP: 94304-1013
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/911, 853
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/639, 092
 FILING DATE: 16-AUG-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Glaister, Debra J
 REGISTRATION NUMBER: 33, 988
 REFERENCE/DOCKET NUMBER: GC361-2
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 650-846-7620
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17612 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-911-853-29

alignment_scores:
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 Ratio: 0.682 Gaps: 34
 Percent Similarity: 42.550 Percent Identity: 22.350

Align seg 1/1 to: US-08-911-853-29 from: 1 to: 17612

58 MetGlnArgAsnLeuLysArgLysLeuSerGlyAlaGlnLeuLe 74
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 7046 ATATGGCCATGCCCTCCGGAGGGGGGGGGGGGGCAACTG 7095
 :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 74 uSerPheSerLysLeuProGlu...PrThrSerGlyValLeuAla... 88
 :::::|||||:|||||:|||||:|||||:|||||:|||||:
 7096 CTTAATCTCCGCTGCGAAAGCCGCAAGGAACCCATTAGTACAA 7145
 :::::|||||:|||||:
 89 ...ArgGalaAlaGluLeMetGluThrSerIleGlnAlaMetLysArgLys 104
 :::::|||||:
 7146 GAAAATCGGGAGATATGCCANGTCAGTTGGTCACGTGGCGGGCT 7195

8613 CGAGCGGGGTCTCGCGACTAACGAGTTCCCGAGATGGCCCTCA 8662
 601 roArgLeuGluThrProAlaAspLeuSerThrAlaLeuAlaArgSer 617
 8663 ACCGATACCAAGTGGAGGACTGACCCACGGCCACCTGGCC 8712
 618 ValAlaAspLysIleLeu.....AspLeuTyrlsProAspAsnI 632
 8713 AACCTCAAGCATACTAGCAAAAGACATGAGAAG.....AT 8750
 632 eAspValTrpLeuGlyLeuAlaGluAsnPhoLeuPro 645
 8751 TGACACCCGGCTGGCATGTCGCCGAGACCGTGCGTCG 8790

seq_name: /cgn2.6/ptodata/2/ina/6A_COMB.seq:US-08-911-853-16

seq_documentation_block:
 Sequence 16, Application US/08911853
 Patent No. 6048710
 GENERAL INFORMATION:
 APPLICANT: Gerritse, Gijbert
 APPLICANT: Quax, Wilhelmus J.
 TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
 TITLE OF INVENTION: EXPRESSION LEVELS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Generon International
 STREET: 925 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1013

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/911,853
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/699,092
 FILING DATE: 16-AUG-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Glaister, Debra J.
 REGISTRATION NUMBER: 33,888
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-846-7620
 TELEFAX: 650-845-6504
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2742 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-911-853-16

alignment_scores:
 Quality: 195.00 Length: 587
 Ratio: 0.789 Gaps: 25
 Percent Similarity: 42.078 Percent Identity: 22.147

alignment_block:
 US-08-482-402A-3_COPY_1_848 x US-08-911-853-16 ..
 Align seg 1/1 to: US-08-911-853-16 from: 1 to: 2742

145 ThrCysLeuAlaAsnLysTyr.....ArgProIleThrGlyAlaCysAs 159
 151 ACCTGTATGCCGAGCCAGGCAAGGGTACGGAGCAGGACCTGTA 200

441 IglyAlaLeuHisGlnIleIleThrLeuArgAspTyrileProArgIleL 458

159 nAsnArgAspHisProArgTrpGlyIalaSerAsnThrAlaLeuAlaArgT 176
 201 CATCCCTGCGRACCCGGCAGGCGCTGGCTGACCCGGCTGGCGCA 250
 176 rPheProProValtyrGluAspGlyPheSerGlnProArgGlyTrpAsn 192
 251 ACGTCGFACCCCAGCCATGGGAGACGCC 288
 193 ProGlyPheLeutyrasnGlyPheProLeuProProValArgGluValTh 209
 289GACACCCGCTGCTAGTCCAATCGCGAGGTGAG 323
 209 rArgHisValIleGlnValSerAsnGluValThrAspaspAspArgT 226
 324 T...AACGTGCTGATGGCGCTGGCGAG 417
 seq_2.6/ptodata/2/ina/6A_COMB.seq:US-08-911-853-16
 226 yrSerAspLeuMetAlaTrpGlyGlnTyrlleasnPhiAsp...Ile 241
 368 TCAACTTCATGCCGCTCCMGGATCAGTCATGGCANGACTGGTC 417
 242 AlaphethrProGinSerThrSerlysAlaAlaPheGlyGlySerAs 258
 418 GAACACGGCCCAACCGGAGCCAAC 444
 258 pCysGlnMetThrCysGluAsnProCysPheProleGlnLeuP 275
 445CCGATCCAGTC 457
 275 roGluAlaArgProAlaAlaGlyThrAlaCysLeuProPhiTyRArg 291
 458 CGCTGGGGTGGCGACGCCCTGGCTCCGGCAGGCTGTGGCCGC 507
 292 SerSer.....AlaAlaCysGlyThrGlyAspG1 301
 508 ACCCAAGCCCACCCGACCGTACCCGGCAGGGGGC 546
 301 nGlyAlaLeuPheGlyAsnLeuSerThrAlaAsnProArgGlnGlnMetA 318
 547AAAGCGGCACCTACCGCA 565
 318 snglyLeuthrSerPhiLeuAspLaserThrvaltyrGlyserSerPro 334
 566 ACCAACACCCACTGGGATGGCTGZGTTGATGGCAGGCCAAAG 615
 335 AlaLeuGluArgGlnLeuArgAsnTrpThrSerAlaGluGlyLeuLeuAr 351
 616 GACATCAACCACAAGTGCGC 648
 351 gValHisGlyArgLeuArgAspSerGlyArgAlaLysThrLeuProPhiValP 368
 649GGAAAGCTGAAGTC 663
 368 roProArgAlaProAlaCysAlaProGlyLysProGlyGlu 384
 664ATICCCGACGGT 675
 385 ThrArgGlyProCysPhiLeuAlaGlyAspGlyArgAlaSerGluValPr 401
 676 ACCCTGGCCGACCGAGTTCCAGCGCAAG.....CC 707
 401 O.....SerieIeHrAlaLeuHist 408
 708 GATCACCGGGTTCAACGAGAACTGGTGGCTGAGCATGCGAC 757
 408 hrLeutrpLeuArgGluHisAsnArgLeuAlaAlaLeuLysAlaLeu 424
 758 AGCTGTTCACTAAGGAGCACACGCCATCCGGCATGCTCCAGCAGAAG 807
 425 AsnAlaHistrpSerAlaAspAlaValtyrGlnGluAlaArgLysVala 441
 808 TACCGGACAGGAGACCCGAGCTGGCTGAGCATGCGCCCTGGTCAA 857

APPLICATION NUMBER: US/08/459,493
 FILING DATE: 08/08/459,493
 PRIORITY APPLICATION DATA:
 CLASSIFICATION: 435
 APPLICATION NUMBER: US 08/080,221
 FILING DATE: 21-JUNE-1983
 TELECOMMUNICATION INFORMATION:
 APPLICATION NUMBER: US 07/746,941
 FILING DATE: 19-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Kohn, Kenneth I.
 REGISTRATION NUMBER: 30,955
 REFERENCE/DOCKET NUMBER: VU9115
 TELEPHONE: (313) 456-8000
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1920 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: cDNA to mRNA
 FEATURE: mat_peptide
 LOCATION: 165..1892
 FEATURE: sig_peptide
 LOCATION: 93..164
 FEATURE: mRNA
 LOCATION: 1..1920
 US-08-459-493-2

alignment_scores:
 Quality: 185.00 Length: 472
 Ratio: 0.801 Gaps: 18
 Percent Similarity: 48.941 Percent Identity: 20.975

alignment_block:
 US-08-482-402A-3_COPY_1-848 x US-08-459-493-2 ..
 Align seg 1/1 to: US-08-459-493-2 from: 1 to: 1920

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 592 GGAAAGCAATTGGCCACATGGGGAGTCCTGCCGCTGCCTGC 641

264 uAsnGlnAsnPro5PhePro6GlnLeuProGluAlaArgProA 281
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 642 AGGAGGAAGTCACTCCGTACCCCAAGGCCACCA..... 675

281 LalaGlyThra1CysLeu2ProPhe3rArgSerSerAlaAlaCysGly 297
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 676ACCTCATGTTGCCCTCTTGCCCAAAACATTCACCATCAGT 717

298 ThrolyAspGlnGlyAlaLeuPheGlyAsnLeuSerThrAlaAsnProA 314
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 718 TCTCAAACCTCGGGAGATG.....GTCCTGGCTACCAAG 758

314 gGlnGlnMetAsnGlyLeuThrSerPheLeuAspAlaSerThrValTyrg 331
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 759 GCCTGGCCACGGGTAGACCTGGCCACATTATGGACAACTCGG. 807

331 lYSerSerProAlaLeuGluArgGlnLeuArgAsnTriPheSerAlaGlu 347
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348 GlyLeuLeuArgVal1.HisGlyArgLeuArgAspSerGlyArgAlaTyrl 364
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 826 GGCTCTTAAGGGGGAGC1GAAGTACAGATGCTAATGGAGAGGTG 875

364 euProPheValProArgAlaProAlaAlaCysAlaProGluProGly 380
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 1662 GAAATGGGGCTCCCTTAAGGGCTCTAGAAACCCATCTG 1711

876 TACCCGCCATGGTGGAAAGGGGCCGCTGCTGATGCACATACCCCCGGGG 925
 381 AsnProGlyGluThrArgGlyProCysPheLeuAlaGlyAspGlyArgAl 397
 926 CATCCGCCCAAGCCAGATGGCTGT.....GGCCAGGAGGTG 966
 397 a . SerGluVal ProSerLeuThrAlaLeuHisThrLeuTerPheLeuArgGlu 413
 967 TGGGGTGCCTCTGGCTCATGCCTACGCCAGACTGGCTGCTGCTGAG 1016
 414 HisAsnArgLeuAlaAlaLeuLysAlaLeuAlaAlaHistPheSerAl 430
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 1017 CACACCCGGTGTGACCTCTGTGAAGGTAGCACCCCACCTGGGGGA 1066
 430 aaspAlaValItyrGlnGluAlaArgLysVal...ValGlyAlaLeuHisG 446
 1067 CGAGCAGCTCTCCAGACGGCCGCTCATCCTCATCGGGAGACCATCA 1116
 446 InIleLeuThrLeuArgAspStrylIleProArgIleLeuGlyProGluAla 462
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 1125 ATAGAGGAGPATGTGACGTGCTGAGCGCTACTCTGCAGCTCAAGT 1174
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 1175 CGACCCAGAGTGTGCTCCAGTCGGG...GCCCAAGTCCAGTACCGCAACCGC. 1220
 496 hrleHisProLeuValArgArgLeuAspAlaSerPheGlnGluHisPro 512
 1221 ATCGCCTATGAGTTAACAGCTGACCATGGCACCCG 1259
 513 AspLeuProGlyLeu..... 522
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 555 LeuMetAsnGlnIgGluLeuIgGluLeuIgLeuLeuValLeuSerAsnSerIe 571
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 1410 ATAGACCACACATCTGCAGTCAGTGGCCGTGATGTCTAGGAATCAGC 1459
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 1460 GGTGCTGAGGTGCAGCCCTCAATGATGTAACGCAAGAGG...TTRNGCA 1506
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 638 IyLeuAlaGluAsnPheLeuProArgAla..... 647
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 1612 TACTCTTGACAGTCGACATCGAATCCACTCTTGGGAGAGTATGATA 1661
 648 ArgThrGlyProLeuPheAlaCys.....LeuIleGlyLysGlnMetLy 662
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662 sAlaLeuArgAspGlyAspTrpPheTrpTrpPheTrpAsnSerHisValPheT 679
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 1712 TTCTCCAGG.....TACTGGAGGCACATTTCGGG 1746

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seq_name: /cgn2_6/podata/2/ina/5B_COMB.seq:us-08-627-254C-26

seq_documentation_block:
 Sequence 26, Application US/08627254C
 Patent No. 5859229
 GENERAL INFORMATION:
 APPLICANT: Kniss, Douglas A.
 TITLE OF INVENTION: Eicosanoid Formation
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Calfee, Halter & Griwold LLP
 STREET: 800 Superior Avenue
 CITY: Cleveland
 STATE: Ohio
 ZIP: 44114
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/627,254C
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Golrick, Mary E.
 REGISTRATION NUMBER: 34,829
 REFERENCE/DOCKET NUMBER: 18525/00107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (216) 622-8200
 TELEFAX: (216) 241-0816
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2757 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-627-254C-26

alignment_scores:
 Quality: 178.50 Length: 698
 Ratio: 0.553 Gaps: 42
 Percent Similarity: 46.275 Percent Identity: 21.633

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151 rArgProfileThrAlaCys.....AsnAsnArgAspH 163
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271 orleGlnLeuProGluGluAla.....ArgP 280
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 272 CAGCTCCGGCCGGCTTCTGTCAAGGAAGTCATACCTGACCC 574
 280 roAlaAlaLgylThrAlaCysLeuProPhetyrArgSerSerAlaAlaCys 296
 275 CCAAGGCCAACCTCATGTTGCTCTTGCACAACTACCCCCACC 624
 297 GlyThrGlyAspDnglyAlaLeuSerThrAlaAsnPr 313
 625 AGTCTCT.....TCAAAACCTCTGCGCAAGATGGTCCTGCTCACCC 665
 313 oArgGlnGlnMetAsnGlyLeuThrSer.....PhleuAspAla Ser 327
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 341 ...ArgAsnTrpThrSerAlaGlyLeuLeuArgValHisGlyArgL 356
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 371 AlaProAlaAlaCysAlaProGluProGlyAlaProGlyGluThrArgG1 387
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 404 ThraAlaLeuHisthrLeuThrLeuArgGluHisAsnArgLeuAlaAlA 420
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 420 alaLysAlaLeuAsnAlaHisthrSerAlaAlaValtyrGlnGluA 437
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 947 GCTGAAGGCTGAGCAACCCACCTGGGGCATGAGCAGTTTCAGACGA 996
 437 LahLyVal...ValGlyAlaLeuIleGlnIleLeuLeuArgAsp 452
 :
 997 CCCGCCATCCATAGGGACACCATCAAGATGFC...ATCGAGGAG 1043
 453 TyrileProArgIleLeugly.....ProG1 461
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 1044 TACGTGCAAGCAGGTAGGGTATTCCTGCAAGCTGAAATTGACCCAGA 1093
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 1094 GCTGCTGTTGGTCCAGTTCCAAATACCGC. 1124
 478 snProThrValSerAsnValPheSerThrAlaAlaPheArgPheGlyHis 494
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 495 AlaThrIleHisProLeuValArgArgLeuAspAlaSerPheGlnGluHi 511
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 1152 CRC. 1165
 511 sProAspLeuProGlyLeu.....TrieLeuAspPro 521
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 1166 CCCCTCATGCCGACTCTTCAAAGTGGCTCCAGGATCAGCTACG 1215
 521 InAlaPhePheSerProTrpThrLeuLeuArgGlyGlyLeuAspPro 537
 | :
 1216 AGCAATGTCAGCTAACACCTCCATGTTGGTGGACTATGGGTTGAGGCC 1265

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq.US-08-487-753-6
 seq_documentation_block:
 Sequence 6, Application US/08487753
 ; GENERAL INFORMATION:
 ; Patent No. 5807733
 ; APPLICANT: Young, Donald A.
 ; APPLICANT: O'Banion, Michael K.
 ; APPLICANT: Winn, Virginia D.
 ; TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,753
 FILING DATE: 07 JUN 1995
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 3996-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEX: 66141 PENNIE
 ID NO: 6
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1819 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 US-08-487-753-6

alignment_scores:
 quality: 171.00 Length: 509
 Ratio: 0.728 Gaps: 25
 Percent Similarity: 46.169 Percent Identity: 21.415

alignment_block:
 US-08-482-402A-3_COPY_1_848 x US-08-487-753-6 ..
 Align seg 1/1 to: US-08-487-753-6 from: 1 to: 1819

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 504 GGAGAAAGCACTGGTCCAGATG.....CC 526

271 GlleGlnLeuProGluGluAla.....ArgP 280
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 527 CAGGCCCTGGCCCGCCTGGTCATACCTGACCC 576

280 roAAAlaAaglyThrAlaCysLeuProPheTyraGserSerAlaAlaCys 296
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 577 CCAAGCACCAACCTCATCTTGCTCTTGCCTCAACACTTCCCCACC 626

297 GlyThrGlyAspGlnGlyAlaLeuPheGlyAsnLeuSerThrAlaAsnPr 313
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 627 AGTCT.....TCATAACTCTGGCAAGTGGTCTGGCTTACCC 667

313 oArgGlnGlnMetAsnGlyLeuThrSer.....PhLeuAspAla.Ser 327
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 668 AAGGCCCTGGCCATTGGGTAGACCTCGGCCACATTGGAGCAATCT 717

328 ThrValTyGlySerSerProAlaLeu.....GluArgGlnLeu .. 340
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 718 GGACGTCAGTATAAACCTGGCTCTTAAGGAGGGAAACTCAAGTACCT 767

341 ...ArgAsnTrpThrSerAlaGluGlyLeuLeuArgValHisGlyArgL 356
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 768 AGGGCTGGATGGAAATGACCGCCCTC..... 798

356 euArgAspSerGlyArg.....AlaTyLeuProPheValProProArg 370
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 799GTTAAAGAGGCCCTGTGTGCACTACCCCGAGG 837

371 AlaProAlaAlaCysAlaProGluProGlyAsnProGlyGluThrArgL 387
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404 ThraAlaLeuHisthrLeuTrpLeuArgGluHiSasnArgLeuAlaAla 420
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899 ATGCTGTATGCCACGGCTCTGGCTACGTGAGCACAAACCGTGTGTGACCT 948
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437 laArgLysval .. ValGlyAlaLeuHisGlnLeilethrLeuArgAsp 452
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 999 CCCGCCCTCATCCATCATGGGAGACCATCAAAGATTC 1045

453 TyrIleProArgIleLeuGly..... 461
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478 snProThrValSerAsnValPheSerThrAlaAlaPheArgPheGlyHis 494
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495 AlaThrIleHisProLeuValArgArgLeuAspAlaSerPheGlnGluHi 511
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 1154 CTC.....TACCACTGGCA 1167

511 sProAspLeuProGlyLeu.....TrpLeuHisG 521
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521 InAlaPhePheSerProTrpThrLeuArgGlyGlyLeuAspPro 537
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538 LeuIleArgGlyLeuLeuAlaArgProAlaLysLeuGlnValGlnAspG 554
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 1268 CTGGTG.....GA 1275

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 1326 ACCACCCACATCTGGCATGCTGGGATGTCATCAGGGAGCTCGGGG 1375

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 :|||:|||:|||:
 1376 ATGGGACTGCAAGCCCTTCATAATGTAACCGCAGAGGGTTGGCATGAAAC 1425

602 gLeuGluThrProAlaAspLeuSerThrAlaLeuSerArgSerValA 619
 :|||:|||:|||:
 1426 CTACACTCTCCATCCAGGAGTC..... 1466

619 lAspLysIleLeuAspLeuArgLysHisPraAspAlileaspValItrP 635
 :|||:|||:|||:
 1467 CAGCAGATGTTGGAGGAATTGTGAGACATGATGCGTGGAGTTCTAC 1516

636 LeuGlyGlyLeuAlaGluAsnLeuProArgAla..... 647
 :|||:|||:|||:
 1517 CCTGGACTGCTCTGAAAGTGGCCATCAAACCTCTATCTTGGGGAGA 1566

648ArgThrGlyProLeuPheAlaCys LeuIleGlyIysG 660
 :|||:|||:|||:
 1567 TATGATAGAATGGGGCTCTCCCTCAAGGGTCTCCPAGGGATAC 1616

660 InMetLysAlaLeuArgAspGlyAspTrPheTrpPheTrpGluAsnSerHis 676
 :|||:|||:
 1617 CCATCCTGTTCTCGGGAG.....TACTSGAAGCGAGGACAA 1651

677 ValPheThrAspAlaGlnArgArgGluLysHisSerLeuSerAla 693

11276	TGCCCTTCCTCGCAGATTGCTGCCGGATCGTGGGGCAGGAACATGG	1325
571	er.....ThrLeuAspLeuAlaSerIleAsnLeuIglnArgGlyArgAsp	585
1326	ACCACCATCCGTCATGGCTGATGTCAGGGAGTCAGGGGAGTCGGGRG	1375
586	HisGlyLeuProGlyTyrosineGluTrpArgGluPheCysCysLeuproAR	602
1376	ATGGGGCTGAGGCCCTCATGGTACCCAAAGGGTTGGCATGAAACC	1425
602	gLeuGluThrProAlaAspLeuSerThrAlaIleAlaSerArgSerValA	619
1426	CTAACACCTCCCTTCAGGAGCTC.....	1466
619	IaAspLysIleLeuAspLeuItyRlyShtisProAspAsnIleAspValItrP	635
1467	CAGCAGCTGGGGAGATGTAATGAGATGAGATGAGATGAGATGAGCTAC	1516
636	LeuGlyGlyLeuAlaGluAsnpheLeuProGala.....	647
1517	CCTGGACTGCTTGTAAAATGTCATCCAAACITATCTTGAGGAGAG	1566
648ArgThrGlyProIlePheAlaCys.....LeuIleGlyLysG	660
1567	TATGATAGAATGGGGTCCCCTTTCCTCAAGGGTCTCTAGGGAAATC	1616
660	InMetLysAlaLeuArgAspGlyAspTrpPheTrpGluAsnSerHis	676
1617	CCATTCTGTTCTCGGGAG.....	1651
677	ValPheThrAspAlaIglnArgArgGluIleGluLysHissLeusSerAR	693
1652	TGGGGCAGGGAGGTGGCTTAAATGTCAAGAGGCCACACTGAAGAA	1701
693	gValIleCysAspAsnThrGlyLeuThrArgValProMetAspAlaPheG	710
1702	GCTGGTGTGCGCTTAACACCC.....AAGACCTGTCCCTACGGTTTCCTCC	1745
710	InValGlyLysPheProGluAsp	717
1746	GTTGCGGGATGAGCACTAGGG.....	1768